

WYS-018.04 -- SEQLIST.TXT
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Freeman, Gordon J.
Nadler, Lee M.
Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 WITH INCREASED IMMUNOGENICITY AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Foley Hoag
(B) STREET: 155 Seaport Boulevard
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10/767,561
(B) FILING DATE: 28-JAN-2004
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/101,624;
(B) FILING DATE: 26-JUL-1993;
(A) APPLICATION NUMBER: 08/109,393;
(b) FILING DATE: 19-AUG-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Russell, Hathaway P.
(B) REGISTRATION NUMBER: 46,488
(C) REFERENCE/DOCKET NUMBER: WYS-018.04

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 832-1000
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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(A) NAME/KEY: CDS
 (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACAGGGTGA AAGCTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
GAGTGGGGTC ATTTCCAGAT ATTAGGTAC AGCAGAACCA GCTAAA ATG GAT CCC Met Asp Pro	115
1	
CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	163
5 10 15	
CTC TCT GGT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	211
20 25 30 35	
GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	259
40 45 50	
GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	307
55 60 65	
GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	355
70 75 80	
GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	403
85 90 95	
CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	451
100 105 110 115	
AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	499
120 125 130	
GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	547
135 140 145	
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gln Tyr	595
150 155 160	
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	643
165 170 175	
ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	691
180 185 190 195	
CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	739
200 205 210	

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AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu 215 220 225	787
TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro 230 235 240	835
GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys 245 250 255	883
GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg 260 265 270 275	931
CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu 280 285 290	979
AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser 295 300 305	1027
GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp 310 315 320	1075
AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCC AAAAAAAA Lys Ser Asp Thr Cys Phe 325	1120

(3) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met 1 5 10 15
Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe 20 25 30
Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln 35 40 45
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val 50 55 60
Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser 65 70 75 80
Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg 85 90 95

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Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile
100						105						110			
His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser
115						120					125				
Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile
130						135					140				
Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile
145						150				155					160
His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys
	165								170					175	
Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn
	180							185					190		
Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro
	195						200					205			
Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys
	210					215					220				
Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln
	225					230				235					240
Pro	Pro	Pro	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val
	245						250					255			
Ile	Ile	Cys	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys
	260						265					270			
Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu
	275						280					285			
Arg	Glu	Glu	Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro
	290					295					300				
Glu	Arg	Ser	Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser
	305					310				315					320
Ser	Cys	Asp	Lys	Ser	Asp	Thr	Cys	Phe							
						325									

(4) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 99..1028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGAGCAAGCA GACCGCTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT	60
CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC Met Asp 1	104
CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu 5 10 15	152
CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly 20 25 30	200
ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu 35 40 45 50	248
AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr 55 60 65	296
GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr 70 75 80	342
CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His 85 90 95	382
AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys 100 105 110	440
AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu 115 120 125 130	488
TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn 135 140 145	536
GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly 150 155 160	584
CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn 165 170 175	632
GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu 180 185 190	680
TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp 195 200 205 210	728
CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser 215 220 225	776
TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT	814

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Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr			
230	235	240	
TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG			872
Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Val Met			
245	250	255	
CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC			920
Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro			
260	265	270	
AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG			968
Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu			
275	280	285	290
ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA			1016
Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro			
295	300	305	
AAT GCA GAG TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT			1065
Asn Ala Glu			
TTGCCTGAAA TAAGAACGTGC AGAGTTCTC AGAATTCAA AATGTTCTCA GCTGATTGGA			1115
ATTCTACAGT TGAATAATTAA AAGAAC			1151

(5) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr				
1	5	10	15	
Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe				
20	25	30		
Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile				
35	40	45		
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val				
50	55	60		
Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala				
65	70	75	80	
Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg				
85	90	95		
Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile				
100	105	110		
Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr				
115	120	125		

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Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
130 135 140

Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
145 150 155 160

Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
165 170 175

Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
180 185 190

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
195 200 205

Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
210 215 220

Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
225 230 235 240

Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu
245 250 255

Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
260 265 270

Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
275 280 285

Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
290 295 300

Lys Pro Asn Ala Glu
305

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACCA TCTCAGAAGT 60

GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT 120

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GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTT	180
GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT	240
TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTGAC	300
CCTAACATC TGAAGGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC	353
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser	
-30	-25
AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT	401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu	
-20	-15
-10	
TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA	449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu	
-5	1
5	10
GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA	497
Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala	
15	20
25	
CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG	545
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met	
30	35
40	
ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC	593
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile	
45	50
55	
TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA	641
Phe Asp Ile Thr Asn Ash Leu Ser Ile Val Ile Leu Ala Leu Arg Pro	
60	65
70	
TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC	689
Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp	
75	80
85	90
GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT	737
Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala	
95	100
105	
GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT	785
Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn	
110	115
120	
ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC	833
Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His	
125	130
135	
CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA	881

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Leu	Ser	Trp	Leu	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr		
140				145					150								
																929	
GTT	TCC	CAA	GAT	CCT	GAA	ACT	GAG	CTC	TAT	GCT	GTT	AGC	AGC	AAA	CTG		
Val	Ser	Gln	Asp	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu		
155					160				165							170	
																977	
GAT	TTC	AAT	ATG	ACA	ACC	AAC	CAC	AGC	TTC	ATG	TGT	CTC	ATC	AAG	TAT		
Asp	Phe	Asn	Met	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr		
				175				180					185				
																1025	
GGA	CAT	TTA	AGA	GTG	AAT	CAG	ACC	TTC	AAC	TGG	AAT	ACA	ACC	AAG	CAA		
Gly	His	Leu	Arg	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln		
				190			195					200					
																1073	
GAG	CAT	TTT	CCT	GAT	AAC	CTG	CTC	CCA	TCC	TGG	GCC	ATT	ACC	TTA	ATC		
Glu	His	Phe	Pro	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile		
				205			210					215					
																1121	
TCA	GTA	AAT	GGA	ATT	TTT	GTG	ATA	TGC	TGC	CTG	ACC	TAC	TGC	TTT	GCC		
Ser	Val	Asn	Gly	Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala		
				220			225				230						
																1169	
CCA	AGA	TGC	AGA	GAG	AGA	AGG	AGG	AAT	GAG	AGA	TTG	AGA	AGG	GAA	AGT		
Pro	Arg	Cys	Arg	Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser		
				235			240				245			250			
																1221	
GTA	CGC	CCT	GTA	TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA													
Val	Arg	Pro	Val														
																1281	
GGTAGCCTCC	GTCATCTCTT	CTGGGATACA	TGGATCGTGG	GGATCATGAG	GCATTCTTCC											1341	
CTTAACAAAT	TTAACGCTGTT	TTACCCACTA	CCTCACCTTC	TTAAAAACCT	CTTTCAGATT												
																1401	
AAGCTGAACA	GTTACAAGAT	GGCTGGCATC	CCTCTCCTTT	CTCCCCATAT	GCAATTGCT											1461	
TAATGTAACC	TCTTCTTTG	CCATGTTCC	ATTCTGCCAT	CTTGAATTGT	CTTGTCAAGCC												
AATTCAATTAT	CTATTAAACA	CTAATTGAG															
1491																	

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	His	Thr	Arg	Arg	Gln	Gly	Thr	Ser	Pro	Ser	Lys	Cys	Pro	Tyr
				-30					-25					-20	
Leu	Asn	Phe	Phe	Gln	Leu	Leu	Val	Leu	Ala	Gly	Leu	Ser	His	Phe	Cys
				-15				-10						-5	
Ser	Gly	Val	Ile	His	Val	Thr	Lys	Glu	Val	Lys	Glu	Val	Ala	Thr	Leu
-1	1				5					10					
Ser	Cys	Gly	His	Asn	Val	Ser	Val	Glu	Glu	Leu	Ala	Gln	Thr	Arg	Ile
15					20					25					30
Tyr	Trp	Gln	Lys	Glu	Lys	Lys	Met	Val	Leu	Thr	Met	Met	Ser	Gly	Asp
				35					40					45	
Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Ile	Phe	Asp	Ile	Thr
				50				55						60	
Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly
						65		70				75			
Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg
					80		85				90				
Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr
					95		100			105					110
Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile
				115				120					125		
Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu
				130				135				140			
Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp
				145				150				155			
Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	Asp	Phe	Asn	Met
					160		165				170				
Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	Gly	His	Leu	Arg
					175		180			185					190
Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	Glu	His	Phe	Pro
					195				200					205	
Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile	Ser	Val	Asn	Gly
				210				215				220			
Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala	Pro	Arg	Cys	Arg
				225				230			235				
Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser	Val	Arg	Pro	Val
					240				245			250			

(8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mus musculus*
- (D) DEVELOPMENTAL STAGE: germ line
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B lymphocyte
- (H) CELL LINE: 70Z and A20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTT TCAGGTTGTG AAACTCAACC	60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG	120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTCT CGATTTTGT GAGCCTAGGA	180
GGTGCTTAAG CTCCATTGGC TCTAGATTCC TGGCTTC CCC CATCATGTTC TCCAAAGCAT	240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC	290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu	
-35 -30 -25	
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT	338
Lys Phe Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg	
-20 -15 -10	
CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG	386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val	
-5 -1 5	
AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT	434
Lys Asp Lys Val Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp	
10 15 20 25	
GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG	482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu	
30 35 40	
TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG	530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg	
45 50 55	
ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC	578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val	
60 65 70	
CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA	626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg	
75 80 85	

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GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys 90 95 100 105	674
GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala 110 115 120	722
GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro 125 130 135	770
CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr 140 145 150	818
ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln 155 160 165	866
CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys 170 175 180 185	914
TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro 190 195 200	962
GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly 205 210 215	1010
TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys 220 225 230	1058
TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu 235 240 245	1106
ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln 250 255 260 265	1154
ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG Thr Val Phe Leu	1206
GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTCGG ACAACTTGAC	1266
ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1326
CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC	1386
ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA	1446
GCTGTCACTA AAAGGAGAGG TGCCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG	1506
GTGTCTGTGG GAGGCCCTGCC CTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGGG	1566
GGCAGAGGAA AAGTGGGGGA GAGGCCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG	1626

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GTGGGGAAAA CTATGGTTGG GATGTAaaaa CGGATAATAA TATAAATATT AAATAAAAAG 1686
AGAGTATTGA GCAAAAAAAA AAAAAAAA
1716

(9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
-35 -30 -25

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
-20 -15 -10

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
-5 -1 1 5 10

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
15 20 25

Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
30 35 40

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
45 50 55

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
60 65 70 75

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
80 85 90

Tyr Gly Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
95 100 105

Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
110 115 120

Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
125 130 135

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
140 145 150 155

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
160 165 170

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
175 180 185

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp

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190 195 200
Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
205 210 215
Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
220 225 230 235
Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
240 245 250
Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
255 260 265
Phe Leu

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTTAGAGCACA

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCTAAAG

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAATACGACTCACTATAGGG

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAAGGTTCCCTCACAAAG

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACATAAGCCTGAGTGAGCTGG

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGATGAGCAGCATCACAGG

(16) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGAGTGAGTCCGAATAC

(17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GACGAGTAGAACATACAGTG

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 111..1040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCACCGCGTC CGGGAGCAAG CAGACCGCTA AGAGTGGCTC CTGTAGGCAG CACGGACTTG	60
AACAACCAGA CTCCTGTAGA CGTGTTCAG AACTTACGGA AGCACCCACG ATG GAC Met Asp 1	116
CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu 5 10 15	164
CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly 20 25 30	212
ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu 35 40 45 50	260
AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr 55 60 65	308

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GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr 70 75 80	356
CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His 85 90 95	404
AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys 100 105 110	452
AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu 115 120 125 130	500
TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn 135 140 145	548
GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly 150 155 160	596
CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn 165 170 175	644
GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu 180 185 190	692
TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp 195 200 205 210	740
CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser 215 220 225	788
TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr 230 235 240	836
TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met 245 250 255	884
CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro 260 265 270	932
AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu 275 280 285 290	980
ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro 295 300 305	1028
AAT GCA GAG TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT Asn Ala Glu	1077

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TTGCCTGAAA TAAGAAGTGC AGAGTTCTC AGAATTCAA AATGTTCTCA GCTGATTGGA	1137
ATTCTACAGT TGAATAATTAAAGAAC	1163